STIC-Biotech/ChemLib 27217

From: Elliott, George
Sent: Friday, March 31, 2000 1:47 PM
To: STIC-Biotech/ChemLib
Cc: Ousley, Andrea
Subject: FW: seq RUSH search

Please rush.

Thanks,

George

-----Original Message-----
From: Ousley, Andrea
Sent: Friday, March 31, 2000 1:44 PM
To: Elliott, George
Subject: seq RUSH search

George,
Please forward this RUSH sequence search request:

Please search the *public and pending* databases for **Seq. ID No. 1 and 2** of 09/458779. Latterich et al., Sequence and method for increasing protein expression in cellular expression systems.

Thank you
Andrea Ousley
11D04
305-6915

George, the reason is a short docket.

636

Point of Contact:
Barb O'Bryen
Technical Info. Specialist
CM1 12C14 Tel: 308-4291

$%^STN;HighlightOn= ***;HighlightOff=*** ;
LOGINID:Trying 3106016892...Open
ssspta1636axo
Welcome to STN International! Enter x:
STNLOGON timed out

Trying 3106016892...Open

Welcome to STN International! Enter x:x
LOGINID:ssspta1636axo
PASSWORD:
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NEWS	9	Feb 28	Patent Information Now Searchable in CAOLD
NEWS	10	Mar 1	New IMSDIRECTORY Provides Pharma Company Details
NEWS	11	Mar 20	INPADOC: PRODUCER WARNING ABOUT DATA DELAYS
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=> file medline, biosis

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=> s ydr361cp

L1 0 YDR361CP

=> s vesicular fusion factor

L2 0 VESICULAR FUSION FACTOR

=> s vesicular fusion and factor

L3 5 VESICULAR FUSION AND FACTOR

=> d bib ab l3 `-5

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L3 ANSWER 1 OF 5 MEDLINE
AN 97250487 MEDLINE
DN 97250487
TI A conserved domain is present in different families of ***vesicular***
fusion proteins: a new superfamily.
AU Weimbs T; Low S H; Chapin S J; Mostov K E; Bucher P; Hofmann K
CS Department of Anatomy, University of California, San Francisco 94143-0452,
USA.. weimbs@itsa.ucsf.edu
NC T32HL07731 (NHLBI)
R01 AI25144 (NIAID)
R01 AI36953 (NIAID)
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF
AMERICA, (1997 Apr 1) 94 (7) 3046-51.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199707

EW 19970702

=> d bib ab 13 1-5

L3 ANSWER 1 OF 5 MEDLINE
AN 97250487 MEDLINE
DN 97250487
TI A conserved domain is present in different families of ***vesicular*** ***fusion*** proteins: a new superfamily.
AU Weimbs T; Low S H; Chapin S J; Mostov K E; Bucher P; Hofmann K
CS Department of Anatomy, University of California, San Francisco 94143-0452, USA.. weimbs@itsa.ucsf.edu
NC T32HL07731 (NHLBI)
R01 AI25144 (NIAID)
R01 AI36953 (NIAID)
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1997 Apr 1) 94 (7) 3046-51.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199707
EW 19970702
AB We have analyzed conserved domains in t-SNAREs [soluble N-ethylmaleimide-sensitive ***factor*** (NSF) attachment protein (SNAP) receptors in the target membrane], proteins that are believed to be involved in the fusion of transport vesicles with their target membrane. By using a sensitive computer method, the generalized profile method, we were able to identify a new homology domain that is common in the two protein families previously identified to act as t-SNAREs, the syntaxin and SNAP-25 (synaptosome-associated protein of 25 kDa) families, which therefore constitute a new superfamily. This homology domain of approximately 60 amino acids is predicted to form a coiled-coil structure. The significance of this homology domain could be demonstrated by a partial suppression of the coiled-coil properties of the domain profile. In proteins belonging to the syntaxin family, a single homology domain is located near the transmembrane domain, whereas the members of the SNAP-25 family possess two homology domains. This domain was also identified in several proteins that have been implicated in vesicular transport but do not belong to any of the t-SNARE protein families. Several new yeast, nematode, and mammalian proteins were identified that belong to the new superfamily. The evolutionary conservation of the SNARE coiled-coil homology domain suggests that this domain has a similar function in different membrane fusion proteins.

L3 ANSWER 2 OF 5 MEDLINE
AN 92078224 MEDLINE
DN 92078224
TI Characterization of trypsin-sensitive ***factor*** (s) required for endosome-endosome fusion.
AU Colombo M I; Gonzalo S; Weidman P; Stahl P
CS Department of Cell Biology and Physiology, Washington University School of Medicine, St. Louis, Missouri 63110..
NC GM 42259 (NIGMS)

AI 20015 (NIAID)
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1991 Dec 5) 266 (34) 23438-45.
Journal code: HIV. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199203
AB Fusion of endosomes appears to be required at early steps of receptor-mediated endocytosis. These fusion events have been reconstituted using a cell-free assay and have been shown to require both cytosolic and membrane-associated proteins. We report here that trypsinization of endosomes completely inhibited fusion. Addition of untreated cytosol cannot restore fusion of trypsinized endosomes. However, fusion activity is restored by the addition of either untreated vesicles or a high salt extract containing peripheral membrane proteins (KE). KE contains both the membrane-associated ***factor*** (s) required for the reconstitution of fusion using trypsinized endosomes and the factors that are normally provided by the cytosol. The restorative activity of KE was sensitive to trypsin treatment or incubation at 100 degrees C, but was largely N-ethylmaleimide (NEM)-resistant. This and other criteria demonstrated that the trypsin-sensitive ***factor*** is distinct from N-ethylmaleimide-sensitive ***factor*** (NSF), an NEM-sensitive protein involved in ***vesicular*** ***fusion*** , and from other known factors that may participate in membrane fusion events. Preliminary fractionation studies indicate that the restorative activity of KE is associated with one or more high molecular weight proteins. The present study indicates that a novel trypsin-sensitive protein(s) is involved in endosome-endosome fusion. This ***factor*** is membrane-associated and is not found in an active form in cytosol as prepared.

L3 ANSWER 3 OF 5 BIOSIS COPYRIGHT 2000 BIOSIS
AN 1997:221271 BIOSIS
DN PREV199799512987
TI A conserved domain is present in different families of ***vesicular*** ***fusion*** proteins: A new superfamily.
AU Weimbs, Thomas (1); Low, Seng Hui; Chapin, Steven J.; Mostov, Keith E.; Bucher, Philipp; Hofmann, Kay
CS (1) Dep. Anatomy, Univ. California San Francisco, 513 Parnassus Avenue, San Francisco, CA 94143-0452 USA
SO Proceedings of the National Academy of Sciences of the United States of America, (1997) Vol. 94, No. 7, pp. 3046-3051.
ISSN: 0027-8424.
DT Article
LA English
AB We have analyzed conserved domains in t-SNAREs (soluble N-ethylmaleimide-sensitive ***factor*** (NSF) attachment protein (SNAP) receptors in the target membrane), proteins that are believed to be involved in the fusion of transport vesicles with their target membrane. By using a sensitive computer method, the generalized profile method, we were able to identify a new homology domain that is common in the two protein families previously identified to act as t-SNAREs, the syntaxin and SNAP-25 (synaptosome-associated protein of 25 kDa) families, which therefore constitute a new superfamily. This homology domain of approximately 60 amino acids is predicted to form a coiled-coil structure. The significance of this homology domain could be demonstrated by a partial suppression of the coiled-coil properties of the domain profile.

In proteins belonging to the syntaxin family, a single homology domain is located near the transmembrane domain, whereas the members of the SNAP-25 family possess two homology domains. This domain was also identified in several proteins that have been implicated in vesicular transport but do not belong to any of the t-SNARE protein families. Several new yeast, nematode, and mammalian proteins were identified that belong to the new superfamily. The evolutionary conservation of the SNARE coiled-coil homology domain suggests that this domain has a similar function in different membrane fusion proteins.

L3 ANSWER 4 OF 5 BIOSIS COPYRIGHT 2000 BIOSIS
AN 1997:96890 BIOSIS
DN PREV199799396093
TI The role of the NSF/SNAP/SNARE ***vesicular*** ***fusion*** machinery in protein targeting in polarized epithelial cells.
AU Weimbs, T.; Low, S. H.; Chapin, S. J.; Whiteheart, S. W.; Bennett, M. K.; Mostov, K. E.
CS Dep. Anatomy, Univ. California, San Francisco, CA 94143 USA
SO Molecular Biology of the Cell, (1996) Vol. 7, No. SUPPL., pp. 445A. Meeting Info.: Annual Meeting of the 6th International Congress on Cell Biology and the 36th American Society for Cell Biology San Francisco, California, USA December 7-11, 1996
ISSN: 1059-1524.
DT Conference; Abstract; Conference
LA English

L3 ANSWER 5 OF 5 BIOSIS COPYRIGHT 2000 BIOSIS
AN 1992:93507 BIOSIS
DN BA93:50057
TI CHARACTERIZATION OF TRYPSIN-SENSITIVE FACTORS REQUIRED FOR ENDOSOME-ENDOSOME FUSION.
AU COLOMBO M I; GONZALO S; WEIDMAN P; STAHL P
CS DEP. CELL BIOL. PHYSIOL., WASHINGTON UNIV. SCH. MED., 660 SOUTH EUCLID AVE., ST. LOUIS, MO. 63110.
SO J BIOL CHEM, (1991) 266 (34), 23438-23445.
CODEN: JBCHA3. ISSN: 0021-9258.
FS BA; OLD
LA English
AB Fusion of endosomes appears to be required at early steps of receptor-mediated endocytosis. These fusion events have been reconstituted using a cell-free assay and have been shown to require both cytosolic and membrane-associated proteins. We report here that trypsinization of endosomes completely inhibited fusion. Addition of untreated cytosol cannot restored fusion of trypsinized endosomes. However, fusion activity is restored by the addition of either untreated vesicles or a high salt extract containing peripheral membrane proteins (KE). KE contains both the membrane-associated ***factor*** (s) required for the reconstitution of fusion using trypsinized endosomes and the factors that are normally provided by the cytosol. The restorative activity of KE was sensitive to trypsin treatment or incubation at 100.degree. C, but was largely N-ethylmaleimide (NEM)-resistant. This and other criteria demonstrated that the trypsin-sensitive ***factor*** is distinct from N-ethylmaleimide-sensitive ***factor*** (NSF), an NEM-sensitive protein involved in ***vesicular*** ***fusion*** , and from other known factors that may participate in membrane fusion events. Preliminary fractionation studies indicate that the restorative activity of KE is associated with one or more high molecular weight proteins. The present

study indicates that a novel trypsin-sensitive protein(s) is involved in endosome-endosome fusion. This ***factor*** is membrane-associated and is not found in an active form in cytosol as prepared.

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=> s latterich or powell

L4          615 LATTERICH OR POWELL

=> s fusion

L5       136763 FUSION

=> s l4 and l5

L6           10 L4 AND L5

=> s secretory

L7       109575 SECRETORY

=> s l4 and l7

L8            1 L4 AND L7

=> s l6 or l7

L9       109585 L6 OR L7

=> duplicate remove

ENTER L# LIST OR (END):l9

109585 ANSWERS REQUESTED EXCEEDS MAXIMUM ALLOWED OF 50000
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L10           0 L6 AND L8

=> s l6 or l8

L11          11 L6 OR L8

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L12            8 DUPLICATE REMOVE L11 (3 DUPLICATES REMOVED)

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L11 ANSWER 1 OF 11 MEDLINE
AN 1998106182 MEDLINE
DN 98106182
TI Kar9p is a novel cortical protein required for cytoplasmic microtubule orientation in yeast.
AU Miller R K; Rose M D
CS Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544, USA.
NC GM-37739 (NIGMS)
SO JOURNAL OF CELL BIOLOGY, (1998 Jan 26) 140 (2) 377-90.
Journal code: HMV. ISSN: 0021-9525.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199804
EW 19980404
AB kar9 was originally identified as a bilateral karyogamy mutant, in which the two zygotic nuclei remained widely separated and the cytoplasmic microtubules were misoriented (Kurihara, L.J., C.T. Beh, M. ***Latterich*** , R. Schekman, and M.D. Rose. 1994. J. Cell Biol. 126:911-923.). We now report a general defect in nuclear migration and microtubule orientation in kar9 mutants. KAR9 encodes a novel 74-kD protein that is not essential for life. The kar9 mitotic defect was similar to mutations in dhc1/dyn1 (dynein heavy chain gene), jnm1, and act5. kar9Delta dhc1Delta, kar9Delta jnm1Delta, and kar9Delta act5Delta double mutants were synthetically lethal, suggesting that these genes function in partially redundant pathways to carry out nuclear migration. A functional GFP-Kar9p ***fusion*** protein localized to a single dot at the tip of the shmoo projection. In mitotic cells, GFP-Kar9p localized to a cortical dot with both mother-daughter asymmetry and cell cycle dependence. In small-budded cells through anaphase, GFP-Kar9p was found at the tip of the growing bud. In telophase and G1 unbudded cells, no localization was observed. By indirect immunofluorescence, cytoplasmic microtubules intersected the GFP-Kar9p dot. Nocodazole experiments demonstrated that Kar9p's cortical localization was microtubule independent. We propose that Kar9p is a component of a cortical adaptor complex that orients cytoplasmic microtubules.

L11 ANSWER 2 OF 11 MEDLINE
AN 95221414 MEDLINE
DN 95221414
TI Characterization of sialyloligosaccharide binding by recombinant soluble and native cell-associated CD22. Evidence for a minimal structural recognition motif and the potential importance of multisite binding.
AU Powell L D; Jain R K; Matta K L; Sabesan S; Varki A
CS Department of Medicine, University of California at San Diego, La Jolla 92093, USA.
NC GM32373 (NIGMS)
AI29326 (NIAID)
CA01649 (NCI)
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1995 Mar 31) 270 (13) 7523-32.
Journal code: HIV. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)

LA English
FS Priority Journals; Cancer Journals
EM 199507
AB CD22, a B cell-specific receptor of the immunoglobulin superfamily, has been demonstrated to bind to oligosaccharides containing alpha 2-6-linked sialic acid (Sia) residues. Previously, we demonstrated that the minimal structure recognized by this lectin is the trisaccharide Sia alpha 2-6Gal beta 1-4GlcNAc, as found on N-linked, O-linked, or glycolipid structures (***Powell*** , L., and Varki, A. (1994) J. Biol. Chem. 269, 10628-10636).
Here we utilize a soluble immunoglobulin ***fusion*** construct (CD22Rg) to determine directly by equilibrium dialysis the stoichiometry (2:1) and dissociation constant (32 microM) for Neu5Ac alpha 2-6Gal beta 1-4Glc binding. Inhibition assays performed with over 30 different natural and synthetic sialylated and/or sulfated compounds are utilized to define in greater detail specific structural features involved in oligosaccharide-protein binding. Specifically, the critical features required for binding include the exocyclic hydroxylated side chain of the Sia residue and the alpha 2-6 linkage position to the underlying Gal unit. Surprisingly, alterations of the 2-, 3-, and 4-positions of the latter residue have limited effect on the binding. The nature of the residue to which the Gal is attached may affect binding. Bi(alpha 2-6)-sialylated biantennary oligosaccharides are capable of simultaneously interacting with both lectin sites present on the dimeric CD22Rg ***fusion*** construct, giving a marked improvement in binding over monosialylated compounds. Furthermore, data are presented indicating that full-length native CD22, expressed on the surface of Chinese hamster ovary cells, is structurally and functionally a multimeric protein, demonstrating a higher apparent affinity for multiply sialylated compounds over monosialylated compounds. These observations provide a mechanism for strong CD22-dependent cell adhesion despite the relatively low Kd for protein-sugar binding.

L11 ANSWER 3 OF 11 MEDLINE
AN 94314421 MEDLINE
DN 94314421
TI Molecular characterization of clustered variants of genes encoding major surface antigens of human Pneumocystis carinii.
AU Garbe T R; Stringer J R
CS Department of Molecular Genetics, Biochemistry and Microbiology, College of Medicine, University of Cincinnati, Ohio 45267-0524.
NC P01 AI28932 (NIAID)
R01 AI 28471 (NIAID)
SO INFECTION AND IMMUNITY, (1994 Aug) 62 (8) 3092-101.
Journal code: GO7. ISSN: 0019-9567.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Cancer Journals; Priority Journals
OS GENBANK-L27092
EM 199410
AB A 13-kb genomic fragment from human Pneumocystis carinii was cloned as repetitive DNA. The fragment contains a cluster of three related genes, each 3 kb in size, and the 5' end of a fourth gene. The predicted polypeptide of the first gene in the cluster comprises 1,030 amino acid residues with a total molecular mass of 116 kDa. The gene's predicted amino acid sequence bears 32% identity to predicted sequences of recently

described gene fragments of ferret P. carinii, which encode an immunodominant surface glycoprotein (gpA) (P. J. Haidaris, T. W. Wright, F. Gigliotti, and C. G. Haidaris, J. Infect. Dis. 166:1113-1123, 1992), and 36% identity to the predicted sequence of a rat P. carinii major surface glycoprotein gene (msg) (J. A. Kovacs, F. ***Powell*** , J. C. Edman, B. Lundgren, A. Martinez, B. Drew, and C. W. Angus, J. Biol. Chem. 268:6034-6040). DNA hybridization showed that sequences related to the cloned msg genes reside on at least 12 chromosomes of human P. carinii at various degrees of multiplicity and/or homology. Affinity-purified antibodies with specificity to a ***fusion*** protein made from the human P. carinii msgI gene recognized two bands on a Western immunoblot containing total human P. carinii protein; they also recognized ***fusion*** proteins derived from the other two genes of the cluster. Monoclonal antibodies with reactivity to Msg of human P. carinii recognized ***fusion*** proteins produced from two msg genes. ***Fusion*** proteins were also recognized by sera from healthy humans and from patients. The msg genes are candidates for the development of immunotherapy and subunit vaccines for the treatment and prevention of P. carinii pneumonia.

L11 ANSWER 4 OF 11 BIOSIS COPYRIGHT 2000 BIOSIS
AN 2000:120950 BIOSIS
DN PREV200000120950
TI Karyogamy block by heat stress in the fertilization of brown algae.
AU Nagasato, Chikako (1); Motomura, Taizo; Ichimura, Terunobu
CS (1) Faculty of Science, Institute of Algological Research, Hokkaido University, Muroran, 051-0003 Japan
SO Journal of Phycology, (dEC., 1999) Vol. 35, No. 6, pp. 1246-1252. ISSN: 0022-3646.
DT Article
LA English
SL English
AB Karyogamy was inhibited by heat stress in zygotes of Scytosiphon lomentaria (Lyngbye) Link (isogamy), Cutleria cylindrica Okamura (anisogamy), and Fucus distichus subsp. evanescens (C. Agardh) ***Powell*** (oogamy). Although high temperatures did not inhibit migration of the male and female nuclei, nuclear envelope ***fusion*** was blocked. The ultrastructural stage at which karyogamy was inhibited varied among these species. In S. lomentaria, the outer membranes fused with each other, but the inner membranes did not fuse. Partial ***fusion*** of the nuclear envelope occurred in C. cylindrica. In F. distichus, the block of karyogamy at high temperature was incomplete, and nuclear ***fusion*** proceeded gradually. The block to karyogamy in S. lomentaria zygotes was reversible, and karyogamy proceeded when zygotes were transferred from 22degree to 14degree C. Experiments using inhibitors suggested that proteins that might be formed de novo after fertilization do not participate in karyogamy or its inhibition at either 14degree or 22degree C.

L11 ANSWER 5 OF 11 BIOSIS COPYRIGHT 2000 BIOSIS
AN 1998:116187 BIOSIS
DN PREV199800116187
TI Kar9p is a novel cortical protein required for cytoplasmic microtubule orientation in yeast.
AU Miller, Rita K.; Rose, Mark D. (1)
CS (1) Dep. Molecular Biol., Princeton Univ., Princeton, NJ 08544 USA
SO Journal of Cell Biology, (Jan. 26, 1998) Vol. 140, No. 2, pp. 377-390.

ISSN: 0021-9525.
DT Article
LA English
AB kar9 was originally identified as a bilateral karyogamy mutant, in which the two zygotic nuclei remained widely separated and the cytoplasmic microtubules were misoriented (Kurihara, L.J., C.T. Beh, M. ***Latterich*** , R. Schekman, and M.D. Rose. 1994. J. Cell Biol. 126:911-923). We now report a general defect in nuclear migration and microtubule orientation in kar9 mutants. KAR9 encodes a novel 74-kD protein that is not essential for life. The kar9 mitotic defect was similar to mutations in dhc1/dyn1 (dynein heavy chain gene), jnm1, and act5. kar9DELTA dhc1DELTA, kar9DELTA jnm1DELTA, and kar9DELTA act5DELTA double mutants were synthetically lethal, suggesting that these genes function in partially redundant pathways to carry out nuclear migration. A functional GFP-Kar9p ***fusion*** protein localized to a single dot at the tip of the shmoo projection. In mitotic cells, GFP-Kar9p localized to a cortical dot with both mother-daughter asymmetry and cell cycle dependence. In small-budded cells through anaphase, GFP-Kar9p was found at the tip of the growing bud. In telophase and G1 unbudded cells, no localization was observed. By indirect immunofluorescence, cytoplasmic microtubules intersected the GFP-Kar9p dot. Nocodazole experiments demonstrated that Kar9p's cortical localization was microtubule independent. We propose that Kar9p is a component of a cortical adaptor complex that orients cytoplasmic microtubules.

L11 ANSWER 6 OF 11 BIOSIS COPYRIGHT 2000 BIOSIS
AN 1995:253279 BIOSIS
DN PREV199598267579
TI Characterization of sialyloligosaccharide binding by recombinant soluble and native cell-associated CD22: Evidence for a minimal structural recognition motif and the potential importance of multisite binding.
AU Powell, Leland D. (1); Jain, Rakesh K.; Matta, Khushi L.; Sabesan, Subramaniam; Varki, Ajit
CS (1) Cancer Cent. 0063, UCSD Sch. Medicine, La Jolla, CA 92093-0063 USA
SO Journal of Biological Chemistry, (1995) Vol. 270, No. 13, pp. 7523-7532. ISSN: 0021-9258.
DT Article
LA English
AB CD22, a B cell-specific receptor of the immunoglobulin superfamily, has been demonstrated to bind to oligosaccharides containing alpha-2-6-linked sialic acid (Sia) residues. Previously, we demonstrated that the minimal structure recognized by this lectin is the trisaccharide Sia-alpha-2-6Gal-beta-1-4GlcNAc, as found on N-linked, O-linked, or glycolipid structures (***Powell*** , L., and Varki, A. (1994) J. Biol. Chem. 269,10628-10636). Here we utilize a soluble immunoglobulin ***fusion*** construct (CD22Rg) to determine directly by equilibrium dialysis the stoichiometry (2:1) and dissociation constant (32 mu-M) for Neu5Ac-alpha-26Gal-beta-1-4Glc binding. Inhibition assays performed with over 30 different natural and synthetic sialylated and/or sulfated compounds are utilized to define in greater detail specific structural features involved in oligosaccharide-protein binding. Specifically, the critical features required for binding include the exocyclic hydroxylated side chain of the Sia residue and the alpha-2-6 linkage position to the underlying Gal unit. Surprisingly, alterations of the 2-, 3-, and 4-positions of the latter residue have limited effect on the binding. The nature of the residue to which the Gal is attached may affect binding. Bi(alpha-2-6)-sialylated biantennary oligosaccharides are capable of

simultaneously interacting with both lectin sites present on the dimeric CD22Rg ***fusion*** construct, giving a marked improvement in binding over monosialylated compounds. Furthermore, data are presented indicating that full-length native CD22, expressed on the surface of Chinese hamster ovary cells, is structurally and functionally a multimeric protein, demonstrating a higher apparent affinity for multiply sialylated compounds over monosialylated compounds. These observations provide a mechanism for strong CD22-dependent cell adhesion despite the relatively low K-d for protein-sugar binding.

L11 ANSWER 7 OF 11 BIOSIS COPYRIGHT 2000 BIOSIS
AN 1994:406247 BIOSIS
DN PREV199497419247
TI Molecular characterization of clustered variants of genes encoding major surface antigens of human Pneumocystis carinii.
AU Garbe, Thomas R. (1); Stringer, James R.
CS (1) Dep. Molecular Genetics, Biochem. Microbiol., Univ. Cincinnati, P.O. Box 670524, 231 Bethesda Ave., Cincinnati, OH 45267-0524 USA
SO Infection and Immunity, (1994) Vol. 62, No. 8, pp. 3092-3101. ISSN: 0019-9567.
DT Article
LA English
AB A 13-kb genomic fragment from human Pneumocystis carinii was cloned as repetitive DNA. The fragment contains a cluster of three related genes, each 3 kb in size. and the 5' end of a fourth gene. The predicted polypeptide of the first gene in the cluster comprises 1.030 amino acid residues with a total molecular mass of 116 kDa. The gene's predicted amino acid sequence bear,, 32% identity to predicted sequences of recently described gene fragments of ferret P. carinii, which encode an immunodominant surface glucoprotein (gpA) (P. J. Haidaris. T. W. Wright. F. Gigliotti, and C. G. Haidaris. J. Infect. Dis. 166:1113-1123, 1992), and 36% identity to the predicted sequence of a rat P. carinii major surface glycoprotein gene (msg) (J. A. Kovacs, F. ***Powell*** , J. C. Edman, B. Lundgren, A. Martinez, B. Drew. and C. W. Angus, J. Biol. Chem. 268:6034-6040). DNA hybridization showed that sequences related to the cloned msg genes reside on at least 12 chromosomes of human P. carinii at various degrees of multiplicity and/or homology. Affinity-purified antibodies with specificity to a ***fusion*** protein made from the human P. carinii msg1 gene recognized two bands on a Western immunoblot containing total human P. carinii protein; they also recognized ***fusion*** proteins derived from the other two genes of the cluster. Monoclonal antibodies with reactivity to msg of human P. carinii recognized ***fusion*** proteins produced from two msg genes. ***Fusion*** proteins were also recognized by sera from healthy humans and from patients. The msg genes are candidates for the development of immunotherapy and subunit vaccines for the treatment and prevention of P. carinii pneumonia.

L11 ANSWER 8 OF 11 BIOSIS COPYRIGHT 2000 BIOSIS
AN 1994:19248 BIOSIS
DN PREV199497032248
TI Taxonomic revision of the family Psammobiidae (Bivalvia: Tellinoidea) in the Australian and New Zealand region.
AU Willan, R. C.
CS Northern Territory Mus. Atrs Sci., GPO Box 4646, Darwin, NT 0801 Australia
SO Records of the Australian Museum Supplement, (1993) Vol. 0, No. 18, pp. 1-132.

ISSN: 0812-7387.

DT Article

LA English

AB Thirty-seven species of Psammobiidae are recognised in a conchologically-based revision of taxa in the Australian and New Zealand region. Four genera are represented: Asaphis Modeer, 1793; Heteroglypta Martens, 1880; Gari Schumacher, 1817; Soletellina Blainville, 1824. The largest genus, Gari, is divided into nine subgenera: Gari sensu stricto; Psammobia Lamarck, 1818; Gobraeus Brown, 1844; Dysmea Dall, Bartsch & Rehder, 1936; Kermadysmea ***Powell*** , 1958; Psammotaena Dall, 1900; Crassulobia n.subgen.; Psammobella Gray, 1851; Psammodonax Cossmann, 1877. Subgenera are not recognised for any of the other three genera. One new species, Gari (Gobraeus) eos, from the Chesterfield-Bellona Plateau in the Coral Sea is described. Asaphis nana ***Powell*** , 1958, Psammobia flexuosa A. Adams & Reeve, 1850, Psammobia brazieri Tate, 1886 and the genus Ascitellina Marwick, 1928 are excluded from the Psammobiidae as presently defined and transferred to the Tellinidae because all possess lateral teeth in at least one valve. Asaphis nana is possibly a species of Agnomyax Stewart, 1930. Psammobia flexuosa is a junior synonym of Cymatoica undulata (Hanley, 1844). Psammobia brazieri is probably a species of Tellina Linne. Ascitellina may be synonymous with Elliptotellina Cossmann, 1887. Psammobia vitrea Quoy & Gaimard, 1835 is transferred to the Galeommatidae, probably to the genus Scintilla Deshayes, 1856. The region possess the highest species diversity known anywhere for the family. Biogeographically, two faunas are discernible - a considerably larger one towards the north essentially of widespread tropical Indo-west Pacific taxa (24 species), and a much smaller temperate one consisting of taxa endemic to southern Australia (5 species), and to New Zealand (5 species). Only three northern Australian species have limited distribution ranges: Gari eos n.sp.; G. rasilis (Melvill & Standen, 1899); G. gracilenta (E.A. Smith, 1884). The wealth of taxa enabled some preliminary phylogenetic consideration of the family. No autapomorphy emerged amongst the approximately 40 shell characters described for each species. Lack of a posterior flexure is considered symplesiomorphic. Lack of lateral teeth and ***fusion*** of the lower limb of the pallial sinus with the pallial line are synapomorphies that have apparently evolved independently several times (ie, homeoplaseous characters) in the Tellinoidea. The few anatomical studies available are equivocal in regard to relationships within the Psammobiidae and between families of the Tellinoidea. More conchological and anatomical studies are required before phylogenetic relationship within the Tellinoidea, the largest family numerically in the Bivalvia, can be assessed.

=> s powell k/au

L13 155 POWELL K/AU

=> s latterich m/au

L14 12 LATTERICH M/AU

=> s powell k?/au

L15 1011 POWELL K?/AU

=> s latterich m?/au

L16 26 LATTERICH M?/AU

=> s l15 or l16

L17 1036 L15 OR L16

=> s fusion or secretory

L18 243730 FUSION OR SECRETORY

=> s l17 and l18

L19 27 L17 AND L18

=> duplicate remove l19

DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n

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L20 17 DUPLICATE REMOVE L19 (10 DUPLICATES REMOVED)

=> d bib ab l20 1-17

L20 ANSWER 1 OF 17 MEDLINE DUPLICATE 1
AN 1999169010 MEDLINE
DN 99169010
TI Genetic interactions between KAR7/SEC71, KAR8/JEM1, KAR5, and KAR2 during nuclear ***fusion*** in Saccharomyces cerevisiae.
AU Brizzio V; Khalfan W; Huddler D; Beh C T; Andersen S S; ***Latterich*** *** M*** ; Rose M D
CS Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544-1014, USA.
NC GM-37739 (NIGMS)
SO MOLECULAR BIOLOGY OF THE CELL, (1999 Mar) 10 (3) 609-26.
Journal code: BAU. ISSN: 1059-1524.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199906
EW 19990601
AB During mating of Saccharomyces cerevisiae, two nuclei fuse to produce a single diploid nucleus. Two genes, KAR7 and KAR8, were previously identified by mutations that cause defects in nuclear membrane ***fusion*** . KAR7 is allelic to SEC71, a gene involved in protein translocation into the endoplasmic reticulum. Two other translocation mutants, sec63-1 and sec72Delta, also exhibited moderate karyogamy defects. Membranes from kar7/sec71Delta and sec72Delta, but not sec63-1, exhibited reduced membrane ***fusion*** in vitro, but only at elevated temperatures. Genetic interactions between kar7 and kar5 mutations were suggestive of protein-protein interactions. Moreover, in sec71 mutants, Kar5p was absent from the SPB and was not detected by Western blot or immunoprecipitation of pulse-labeled protein. KAR8 is allelic to JEMI, encoding an endoplasmic reticulum resident DnaJ protein required for

nuclear ***fusion*** . Overexpression of KAR8/JEM1 (but not SEC63) strongly suppressed the mating defect of kar2-1, suggesting that Kar2p interacts with Kar8/Jem1p for nuclear ***fusion*** . Electron microscopy analysis of kar8 mutant zygotes revealed a nuclear ***fusion*** defect different from kar2, kar5, and kar7/sec71 mutants. Analysis of double mutants suggested that Kar5p acts before Kar8/Jem1p. We propose the existence of a nuclear envelope ***fusion*** chaperone complex in which Kar2p, Kar5p, and Kar8/Jem1p are key components and Sec71p and Sec72p play auxiliary roles.

L20 ANSWER 2 OF 17 BIOSIS COPYRIGHT 2000 BIOSIS
AN 2000:37961 BIOSIS
DN PREV200000037961
TI Vff2p, a nuclear sec17/sec18 suppressor in vesicular traffic and ***fusion*** .
AU ***Powell, Kendall S. (1)*** ; Patel, Sheetal K. (1); Sun, Ya-Lin (1); ***Latterich, Martin (1)***
CS (1) Salk Institute, 10010 N. Torrey Pines Road, La Jolla, CA, 92037 USA
SO Molecular Biology of the Cell, (Nov., 1999) Vol. 10, No. SUPPL., pp. 298a. Meeting Info.: 39th Annual Meeting of the American Society for Cell Biology Washington, D.C., USA December 11-15, 1999 The American Society for Cell Biology
. ISSN: 1059-1524.
DT Conference
LA English

L20 ANSWER 3 OF 17 MEDLINE DUPLICATE 2
AN 1998165341 MEDLINE
DN 98165341
TI Organelle membrane ***fusion*** : a novel function for the syntaxin homolog Ufe1p in ER membrane ***fusion*** .
AU Patel S K; Indig F E; Olivieri N; Levine N D; ***Latterich M***
CS The Salk Institute, La Jolla, California 92037, USA.
SO CELL, (1998 Mar 6) 92 (5) 611-20.
Journal code: CQ4. ISSN: 0092-8674.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199806
EW 19980601
AB The ***fusion*** of endoplasmic reticulum (ER) membranes in yeast does not require Sec18p/NSF and Sec17p, two proteins needed for docking of vesicles with their target membrane. Instead, ER membranes require a NSF-related ATPase, Cdc48p. Since both vesicular and organelle ***fusion*** events use related ATPases, we investigated whether both ***fusion*** events are also SNARE mediated. We present evidence that the ***fusion*** of ER membranes requires Ufe1p, a t-SNARE that localizes to the ER, but no known v-SNAREs. We propose that the Ufe1 protein acts in the dual capacity of an organelle membrane ***fusion*** -associated SNARE by undergoing direct t-t-SNARE and Cdc48p interactions during organelle membrane ***fusion*** as well as a t-SNARE for vesicular traffic.

L20 ANSWER 4 OF 17 MEDLINE
AN 1998426381 MEDLINE
DN 98426381

TI Expression of snowdrop lectin (GNA) in transgenic rice plants confers resistance to rice brown planthopper.
AU Rao K V; Rathore K S; Hodges T K; Fu X; Stoger E; Sudhakar D; Williams S; Christou P; Bharathi M; Bown D P; ***Powell K S*** ; Spence J; Gatehouse A M; Gatehouse J A
CS Department of Botany & Plant Pathology, Purdue University, West Lafayette, IN 47907, USA.
SO PLANT JOURNAL, (1998 Aug) 15 (4) 469-77.
Journal code: BRU. ISSN: 0960-7412.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199901
EW 19990104
AB Snowdrop lectin (Galanthus nivalis agglutinin; GNA) has been shown previously to be toxic towards rice brown planthopper (Nilaparvata lugens; BPH) when administered in artificial diet. BPH feeds by phloem abstraction, and causes 'hopper burn', as well as being an important virus vector. To evaluate the potential of the gna gene to confer resistance towards BPH, transgenic rice (Oryza sativa L.) plants were produced, containing the gna gene in constructs where its expression was driven by a phloem-specific promoter (from the rice sucrose synthase RSs1 gene) and by a constitutive promoter (from the maize ubiquitin ubi1 gene). PCR and Southern analyses on DNA from these plants confirmed their transgenic status, and that the transgenes were transmitted to progeny after self-fertilization. Western blot analyses revealed expression of GNA at levels of up to 2.0% of total protein in some of the transgenic plants. GNA expression driven by the RSs1 promoter was tissue-specific, as shown by immunohistochemical localization of the protein in the non-lignified vascular tissue of transgenic plants. Insect bioassays and feeding studies showed that GNA expressed in the transgenic rice plants decreased survival and overall fecundity (production of offspring) of the insects, retarded insect development, and had a deterrent effect on BPH feeding. gna is the first transgene to exhibit insecticidal activity towards sap-sucking insects in an important cereal crop plant.

L20 ANSWER 5 OF 17 MEDLINE
AN 1998049938 MEDLINE
DN 98049938
TI Compartment-ablation studies of GLUT4 distribution in adipocytes: evidence for multiple intracellular pools.
AU Millar C A; Campbell L C; Cope D L; Melvin D R; ***Powell K A*** ; Gould G W
CS Division of Biochemistry and Molecular Biology, University of Glasgow, Scotland, U.K.
SO BIOCHEMICAL SOCIETY TRANSACTIONS, (1997 Aug) 25 (3) 974-7. Ref: 25
Journal code: E48. ISSN: 0300-5127.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199803
EW 19980302
AB The available data suggest that GLUT4 does populate the recycling

endosomal system to some extent, but that a large proportion of the intracellular GLUT4 resides in a compartment that is devoid of transferrin receptors and may have properties more akin to specialized ***secretory*** vesicles. The study of the nature and biogenesis of this compartment will provide important insight into the mechanism by which insulin stimulates glucose transport. Further study of the role of the synaptobrevins in these distinct subcellular compartments will probably shed further light on the mechanism by which insulin stimulates GLUT4 translocation.

L20 ANSWER 6 OF 17 MEDLINE DUPLICATE 3
AN 1998030786 MEDLINE
DN 98030786
TI High-affinity binding of the cell cycle-regulated transcription factors E2F1 and E2F4 to benzo[a]pyrene diol epoxide-DNA adducts.
AU Johnson D G; Coleman A; ***Powell K L*** ; MacLeod M C
CS University of Texas M. D. Anderson Cancer Center, Science Park-Research Division, Smithville 78957, USA.
NC E507784
SO MOLECULAR CARCINOGENESIS, (1997 Oct) 20 (2) 216-23.
Journal code: AEQ. ISSN: 0899-1987.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199802
EW 19980204
AB Previous studies indicated that DNA adducts formed by a carcinogenic diol epoxide, 7r,8t-dihydroxy-9t, 10t-epoxy-7,8,9,10-tetrahydrobenzo[a]pyrene (BPDE), can increase the affinity of the transcription factor Sp1 for DNA sequences that are not normally specific binding sites. It was suggested that adduct-induced bends in the DNA were responsible for this behavior. The cell cycle-regulated transcription factor E2F is also known to bend DNA upon binding. When partially purified E2F was tested in a gel mobility-shift assay, binding to a target DNA containing two consensus E2F-binding sites was enhanced by prior modification of the DNA with BPDE. Recombinant human E2F1, E2F4, and DP1 ***fusion*** proteins were affinity purified from bacteria expressing these genes. A combination of either E2F1 or E2F4 with their dimerization partner, DP1, gave preparations that exhibited binding to the E2F site-containing DNA fragment. In both cases, the proteins exhibited much higher apparent affinity for BPDE-modified DNA than for unmodified DNA. In addition, BPDE-modified DNA was a better competitor for the binding than unmodified DNA. Heterologous DNA that contained no consensus E2F binding motifs also competed well for E2F binding when modified with BPDE. In contrast, transcription factor that does not bend DNA appreciably (GAL4) did not show enhanced affinity for BPDE-modified DNA. These findings suggest that numerous transcription factors that bend DNA may bind with anomalously high affinity to sequences that contain carcinogen-DNA adducts.

L20 ANSWER 7 OF 17 BIOSIS COPYRIGHT 2000 BIOSIS
AN 1997:97871 BIOSIS
DN PREV199799397074
TI Protein mediators of ER membrane ***fusion*** .
AU ***Latterich, M.*** ; Patel, S.; Levine, N.; Joaquin, J.
CS Salk Inst., La Jolla, CA 92037 USA

SO Molecular Biology of the Cell, (1996) Vol. 7, No. SUPPL., pp. 614A.
Meeting Info.: Annual Meeting of the 6th International Congress on Cell Biology and the 36th American Society for Cell Biology San Francisco, California, USA December 7-11, 1996
ISSN: 1059-1524.
DT Conference; Abstract; Conference
LA English

L20 ANSWER 8 OF 17 MEDLINE DUPLICATE 4
AN 96016084 MEDLINE
DN 96016084
TI Membrane ***fusion*** and the cell cycle: Cdc48p participates in the ***fusion*** of ER membranes.
AU ***Latterich M*** ; Frohlich K U; Schekman R
CS Howard Hughes Medical Institute, University of California, Berkeley 94720, USA..
SO CELL, (1995 Sep 22) 82 (6) 885-93.
Journal code: CQ4. ISSN: 0092-8674.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199601
AB The ***fusion*** of endoplasmic reticulum (ER) membranes in yeast is an essential process required for normal progression of the nuclear cell cycle, karyogamy, and the maintenance of an intact organellar compartment. We showed previously that this process requires a novel ***fusion*** machinery distinct from the classic membrane docking/ ***fusion*** machinery containing Sec17p (alpha-SNAP) and Sec18p (NSF). Here we show that Cdc48p, a cell-cycle protein with homology to Sec18p, is required in ER ***fusion*** . A temperature-sensitive cdc48 mutant is conditionally defective in ER ***fusion*** in vitro. Addition of purified Cdc48p restores the ***fusion*** of isolated cdc48 mutant ER membranes. We propose that Cdc48p is part of an evolutionarily conserved ***fusion*** /docking machinery involved in multiple homotypic ***fusion*** events.

L20 ANSWER 9 OF 17 BIOSIS COPYRIGHT 2000 BIOSIS
AN 1995:189517 BIOSIS
DN PREV199598203817
TI Membrane traffic early in the ***secretory*** pathway.
AU Schekman, Randy (1); Barlowe, Charles (1); Yeung, Tom (1); Bednarek, Sebastian (1); Salama, Nina (1); ***Latterich, Martin (1)*** ; Hamamoto, Susan (1); Orci, Lelio
CS (1) Dep. Molecular and Cell Biol., Univ. Calif., Berkeley, CA 94720 USA
SO Journal of Cellular Biochemistry Supplement, (1995) Vol. 0, No. 19A, pp. 133.
Meeting Info.: Keystone Symposium on Plant Cell Biology: Mechanisms, Molecular Machinery, Signals and Pathways Taos, New Mexico, USA January 7-13, 1995
ISSN: 0733-1959.
DT Conference
LA English

L20 ANSWER 10 OF 17 MEDLINE DUPLICATE 5
AN 94342409 MEDLINE
DN 94342409
TI Characteristics of endoplasmic reticulum-derived transport vesicles.

AU Rexach M F; ***Latterich M*** ; Schekman R W
CS Department of Molecular and Cell Biology, University of California, Berkeley 94720..
SO JOURNAL OF CELL BIOLOGY, (1994 Sep) 126 (5) 1133-48.
Journal code: HMV. ISSN: 0021-9525.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199411
AB We have isolated vesicles that mediate protein transport from the ER to Golgi membranes in perforated yeast. These vesicles, which form de novo during in vitro incubations, carry lumenal and membrane proteins that include core-glycosylated pro-alpha-factor, Bet1, Sec22, and Bos1, but not ER-resident Kar2 or Sec61 proteins. Thus, lumenal and membrane proteins in the ER are sorted prior to transport vesicle scission. Inhibition of Ypt1p-function, which prevents newly formed vesicles from docking to cis-Golgi membranes, was used to block transport. Vesicles that accumulate are competent for ***fusion*** with cis-Golgi membranes, but not with ER membranes, and thus are functionally committed to vectorial transport. A 900-fold enrichment was developed using differential centrifugation and a series of velocity and equilibrium density gradients. Electron microscopic analysis shows a uniform population of 60 nm vesicles that lack peripheral protein coats. Quantitative Western blot analysis indicates that protein markers of cytosol and cellular membranes are depleted throughout the purification, whereas the synaptobrevin-like Bet1, Sec22, and Bos1 proteins are highly enriched. Uncoated ER-derived transport vesicles (ERV) contain twelve major proteins that associate tightly with the membrane. The ERV proteins may represent abundant cargo and additional targeting molecules.

L20 ANSWER 11 OF 17 MEDLINE DUPLICATE 6
AN 94327707 MEDLINE
DN 94327707
TI Nuclear congression and membrane ***fusion*** : two distinct events in the yeast karyogamy pathway.
AU Kurihara L J; Beh C T; ***Latterich M*** ; Schekman R; Rose M D
CS Lewis Thomas Laboratory, Princeton University, New Jersey 08544..
NC GM37739 (NIGMS)
SO JOURNAL OF CELL BIOLOGY, (1994 Aug) 126 (4) 911-23.
Journal code: HMV. ISSN: 0021-9525.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199411
AB Karyogamy is the process where haploid nuclei fuse to form a diploid nucleus during yeast mating. We devised a novel genetic screen that identified five new karyogamy (KAR) genes and three new cell ***fusion*** (FUS) genes. The kar mutants fell into two classes that represent distinct events in the yeast karyogamy pathway. Class I mutations blocked congression of the nuclei due to cytoplasmic microtubule defects. In Class II mutants, nuclear congression proceeded and the membranes of apposed nuclei were closely aligned but unfused. In vitro, Class II mutant membranes were defective in a homotypic ER/nuclear membrane ***fusion*** assay. We propose that Class II mutants define components of a novel membrane ***fusion*** complex which functions

during vegetative growth and is recruited for karyogamy.

L20 ANSWER 12 OF 17 MEDLINE DUPLICATE 7
AN 94306521 MEDLINE
DN 94306521
TI The karyogamy gene KAR2 and novel proteins are required for ER-membrane ***fusion*** .
AU ***Latterich M*** ; Schekman R
CS Howard Hughes Medical Institute, University of California, Berkeley 94720..
SO CELL, (1994 Jul 15) 78 (1) 87-98.
Journal code: CQ4. ISSN: 0092-8674.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199410
AB We have developed assays using cells and isolated membranes to identify factors mediating ***fusion*** of the ER-nuclear membrane network in yeast. When cells containing distinctly tagged ER-nuclear envelope membranes are observed during mating, the markers of both parental membranes become colocalized in a process sharing a genetic requirement with karyogamy. Using isolated membranes, we find that ***fusion*** between ER compartments requires ATP, but not cytosol, Sec17p (alpha-SNAP), or Sec18p (NSF), the latter two being required at the ***fusion*** step in vesicular transport. Proteins tightly associated with the ER membrane are essential for ***fusion*** , as is Kar2p (BiP), an ER lumenal hsp70 homolog. BiP may activate an ER-localized fusogen, allowing nuclear ***fusion*** and karyogamy in yeast.

L20 ANSWER 13 OF 17 MEDLINE DUPLICATE 8
AN 94089889 MEDLINE
DN 94089889
TI Helicobacter pylori eradication: efficacy and side effect profile of a combination of omeprazole, amoxycillin and metronidazole compared with four alternative regimens.
AU Bell G D; ***Powell K U*** ; Burridge S M; Bowden A N; Rameh B; Bolton G; Purser K; Harrison G; Brown C; Gant P W; et al
CS Department of Medicine, Ipswich Hospital, UK..
SO QUARTERLY JOURNAL OF MEDICINE, (1993 Nov) 86 (11) 743-50.
Journal code: QKZ. ISSN: 0033-5622.
CY ENGLAND: United Kingdom
DT (CLINICAL TRIAL)
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199403
AB We evaluated eradication of Helicobacter pylori infection in 263 patients by a new 14-day regimen of omeprazole 40 mg mane (a gastric ***secretory*** inhibitor) plus two antibiotics: amoxycillin 500 mg three-times daily (tds) plus metronidazole 400 mg tds. The comparative groups included updated results of our previous work with a 14-day course of either standard triple therapy (STT, colloidal bismuth subcitrate 120 mg four times daily (qds) plus tetracycline 500 mg qds and metronidazole 400 mg tds), omeprazole 40 mg once daily plus amoxycillin 500 mg tds (OA), or two modified triple therapy: either Borody's (BTT) of all three components (colloidal bismuth subcitrate 120 mg, tetracycline 500 mg,

metronidazole 200 mg) qds instead of tds, or Logan's (LTT) seven-day therapeutic regimen of colloidal bismuth subcitrate 120 mg qds, amoxycillin 500 mg qds and, for the last three days, metronidazole 400 mg five times daily. Omeprazole/amoxycillin/metronidazole (OAM) therapy was better tolerated than STT (course completion 98.1% vs. 81.4%, $p < 0.001$). H. pylori was eradicated by OAM therapy in 53/55 (96.4%) patients with metronidazole-sensitive organisms and in 54/72 (75.0%) with metronidazole-resistant isolates ($p < 0.01$). The respective corresponding rates for STT and OA therapy were 20/22 (90.9%) and 14/29 (48.3%), (metronidazole-sensitive organisms) and 7/21 (33.3%) and 15/31 (48.4%) (infections resistant to metronidazole). BTT and LTT were also better tolerated than STT. The eradication rate for BTT was 23/26 (88.5%) but that for LTT, the best tolerated of the five treatment regimens, was only 19/28 (67.9%) when pretreatment isolates were metronidazole-sensitive.(ABSTRACT TRUNCATED AT 250 WORDS)

L20 ANSWER 14 OF 17 MEDLINE
AN 88151003 MEDLINE
DN 88151003
TI Structural studies of nerve terminals containing melanin-concentrating hormone in the eel, Anguilla anguilla.
AU ***Powell K A*** ; Baker B I
CS Electron Optics Centre, School of Materials Science, University of Bath, United Kingdom..
SO CELL AND TISSUE RESEARCH, (1988 Feb) 251 (2) 433-9.
Journal code: CQD. ISSN: 0302-766X.
CY GERMANY, WEST: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198806
AB Eels were adapted to black- or white-coloured backgrounds and the pituitary glands were prepared for light and electron microscopy. Immunocytochemical staining was used to study the distribution of the neurohypophysial melanin-concentrating hormone in the neurointermediate lobe. The hormone was located in small, elliptical, electron-opaque neurosecretory granules, measuring approximately 120 x 90 nm. The neurones terminated on blood vessels in the centre of the neurohypophysis and on the basement membrane separating neural and intermediate lobe tissues. The results of both light and electron immunocytochemistry and of radioimmunoassay are consistent with a higher rate of hormone release from eels adapted to white backgrounds than from those adapted to black backgrounds. In addition to this, when fish that had been adapted to white tanks were transferred to black tanks, there was an accumulation of irMCH in the gland and an increased numerical density of ***secretory*** granules at nerve terminals. These results reinforce the proposal that MCH is released during adaptation to a white background, to cause melanin concentration and to inhibit MSH release, and that its release is halted in black-adapted fish.

L20 ANSWER 15 OF 17 MEDLINE DUPLICATE 9
AN 87004565 MEDLINE
DN 87004565
TI Identification of an Epstein-Barr virus-coded thymidine kinase.
AU Littler E; Zeuthen J; McBride A A; Trost Sorensen E; ***Powell K L*** ; Walsh-Arrand J E; Arrand J R
SO EMBO JOURNAL, (1986 Aug) 5 (8) 1959-66.

Journal code: EMB. ISSN: 0261-4189.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198701
AB We have demonstrated the presence of an Epstein-Barr virus (EBV)-coded thymidine kinase (TK) by producing biochemically transformed, TK-positive mammalian cell lines using either microinjection of whole EBV virions or calcium phosphate-mediated transfection of the SalI-B restriction endonuclease fragment of EBV DNA. Analysis of these cell lines showed that: (i) EBV DNA was present in the cell lines, (ii) sequences from the SalI-B restriction endonuclease fragment of EBV were expressed, (iii) a TK activity was present and (iv) a protein with antigenic cross-reactivity with the herpes simplex virus (HSV) TK was produced. The identity of the EBV TK gene was determined by demonstrating that a recombinant plasmid, which expressed the protein product of the BXLF1 open reading frame as a ***fusion*** protein, could complement TK- strains of E. coli. A comparison of the predicted amino acid sequences of the TK proteins of EBV and HSV-1 revealed significant regions of homology.

L20 ANSWER 16 OF 17 MEDLINE DUPLICATE 10
AN 77229163 MEDLINE
DN 77229163
TI Improved method for collection of nasal mucus.
AU ***Powell K R*** ; Shorr R; Cherry J D; Hendley J O
SO JOURNAL OF INFECTIOUS DISEASES, (1977 Jul) 136 (1) 109-11.
Journal code: IH3. ISSN: 0022-1899.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Abridged Index Medicus Journals; Priority Journals
EM 197711
AB Specimens of nasal mucus obtained after stimulaton of the mucosa with water and nasal washings from 20 volunteers were compared for content of IgA. The median concentration of IgA was 70 mg/dl in nasal mucus and 17 mg/dl in nasal washings concentrated 10-fold. The use of nasal mucus should allow for more accurate determination of nasal ***secretory*** antibody activity.

L20 ANSWER 17 OF 17 MEDLINE
AN 72175076 MEDLINE
DN 72175076
TI Effects of secretin and bile salt infusions on canine bile composition and flow.
AU Soloway R D; Clark M L; ***Powell K M*** ; Senior J R; Brooks F P
SO AMERICAN JOURNAL OF PHYSIOLOGY, (1972 Mar) 222 (3) 681-6.
Journal code: 3U8. ISSN: 0002-9513.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 197209